AMENDMENT

Please incorporate the following amendments into the subject application.

In the Claims:

1. (Original) A method of quantifying the amount of a target nucleic acid of less than about 30 nt in length in a sample, said method comprising:

a) contacting said sample with at least two ligation domains that are complementary to different domains of said target nucleic to produce a reaction mixture;

b) ligating any resultant annealed ligation domains of any resultant ligation oligonucleotide/target nucleic acid complexes in said reaction mixture to produce a pseudotarget nucleic acid; and

c) determining the presence of any pseudotarget nucleic acids in said reaction mixture to quantify the amount of said target nucleic acid in said sample.

2. (Withdrawn) The method according to Claim 1, wherein said target nucleic acid is a ribonucleic acid.

3. (Withdrawn) The method according to Claim 1, wherein said target nucleic acid does not exceed about 25 nt in length.

4. (Withdrawn) The method according to Claim 1, wherein said target nucleic acid is single-stranded.

5. (Original) The method according to Claim 1, wherein said target nucleic acid is an siRNA molecule.

6. (Original) The method according to Claim 5, wherein said siRNA molecule is a shRNA molecule.

7. (Withdrawn) The method according to Claim 1, wherein said ligation domains are present on separate oligonucleotides.

8. (Withdrawn) The method according to Claim 7, wherein said ligation domains are present on a Combined Oligo.

9. (Withdrawn) The method according to Claim 8, wherein said Combined Oligo is a linear deoxyribonucleic acid comprising terminal ligation domains.

10. (Withdrawn) The method according to Claim 10, wherein said determining does not comprise amplifying said pseudotarget nucleic acid.

11. (Withdrawn) The method according to Claim 1, wherein said determining comprises amplifying said pseudotarget nucleic acid.

12. (Withdrawn) The method according to Claim 1, wherein said amplifying is by one of PCR, isothermal amplification, rolling circle amplification and branched DNA.

13. (Withdrawn) The method according to Claim 1, wherein said quantifying is relative.

14. (Withdrawn) The method according to Claim 1, wherein said quantifying is absolute.

15. (Withdrawn) The method according to Claim 1, wherein said ligating occurs at a temperature ranging from about 20 to about 45°C.

16. (Withdrawn) The method according to Claim 15, wherein said ligating occurs at a temperature ranging from about 37 to about 42 °C.

17. (Withdrawn) The method according to Claim 1, wherein said target nucleic acid is a peptide nucleic acid, locked nucleic acid, methylated nucleic acid, nucleic acid conjugate, thio-nucleic acid or morpholino nucleic acid.

18. (Original) A method of quantifying an siRNA in a sample, said method comprising:

a) contacting said sample with at least two ligation deoxyribo-oligonucleotides that are complementary to different adjacent domains of said siRNA to produce a reaction mixture;

b) ligating any annealed ligation deoxyribo-oligonucleotides of any resultant ligation deoxyribooligonucleotide/siRNA complexes in said reaction mixture to produce a pseudotarget nucleic acid;

c) amplifying any pseudotarget nucleic acids in said reaction mixture by PCR; and

d) detecting any resultant PCR amplified product to quantitate said siRNA in said sample.

19. (Original) The method according to Claim 18, wherein said siRNA is single-stranded.

20. (Original) The method according to Claim 18, wherein said siRNA is double-stranded.

21. (Original) The method according to Claim 20, wherein said double-stranded siRNA is a short hairpin RNA.

22. (Original) The method according to Claim 18, wherein said quantitating is relative.

23. (Original) The method according to Claim 18, wherein said quantitating is absolute.

24-31 (Canceled)

32. (Previously Presented) The method according to Claim 1, wherein said target nucleic acid ranges in length from about 20 to about 23 nt.

33. (Previously Presented) The method according to Claim 5, wherein said siRNA is a duplex structure which ranges in length from about 15 to about 30 bp.

34. (Previously Presented) The method according to Claim 33, wherein said duplex structure which ranges in length from about 20 to about 29 bp.

35. (Previously Presented) The method according to Claim 34, wherein said duplex structure is 21, 22 or 23 bp in length.

36. (Previously Presented) The method according to Claim 20, wherein said siRNA is a duplex structure which ranges in length from about 15 to about 30 bp.

37. (Previously Presented) The method according to Claim 36, wherein said duplex structure which ranges in length from about 20 to about 29 bp.

38. (Previously Presented) The method according to Claim 37, wherein said duplex structure is 21, 22 or 23 bp in length.